

OIPF

RAW SEQUENCE LISTING DATE: 05/03/2000
 PATENT APPLICATION: US/09/549,342 TIME: 19:47:21

Input Set : A:\5972USP6 SEQ LISTING.txt
 Output Set: N:\CRF3\050300\I549342.raw

Does Not Comply
 Corrected Diskette Needed

P.3

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4 <110> APPLICANT: COLPITTS, Tracey L.
5   RUSSELL, John C.
7 <120> TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR
8   DETECTING DISEASES OF THE REPRODUCTIVE TISSUES
11 <130> FILE REFERENCE: 5972.US.P6
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/549,342
C--> 13 <141> CURRENT FILING DATE: 2000-04-13
13 <150> PRIOR APPLICATION NUMBER: 09/467,602
14 <151> PRIOR FILING DATE: 1999-12-20
16 <160> NUMBER OF SEQ ID NOS: 12
18 <170> SOFTWARE: FastSEQ for Windows Version 3.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 482
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapien
25 <400> SEQUENCE: 1
26 aaatagccct gggctctgca gctccacagg ctccctggggt ggagtccaaa tcactcattg      60
27 ttgtgaaag ctgagctcac agcaaaacaa gccaccatga agctgtcggg gtgtctcctg      120
28 ctggtcacgc tggccctctg ctgctaccag gccaatgccg agttctgccc agctcttggt      180
29 tctgagctgt tagacttctt cttcattagt gaacctctgt tcaagttaag tcttgccaaa      240
30 ttgatgccc ctccggaagc tgttcagacc aagttaggag tgaagagatg cacggatcag      300
31 atgtcccttc agaaacgaag cctcattgcg gaagtcctgg tgaataatatt gaagaaatgt      360
32 agtgtgtgac atgtaaaaac ttctatcctg gtttccactg tctttcaatg acaccctgat      420
33 cttcactgca gaatgtaaag gtttcaacgt cttgctttta taaatcactt gctctccacg      480
34 tc                                                                    482
36 <210> SEQ ID NO: 2
37 <211> LENGTH: 90
38 <212> TYPE: PRT
39 <213> ORGANISM: Homo sapien
41 <400> SEQUENCE: 2
42 Met Lys Leu Ser Val Cys Leu Leu Leu Val Thr Leu Ala Leu Cys Cys
43   1           5           10           15
44 Tyr Gln Ala Asn Ala Glu Phe Cys Pro Ala Leu Val Ser Glu Leu Leu
45   20           25           30
46 Asp Phe Phe Phe Ile Ser Glu Pro Leu Phe Lys Leu Ser Leu Ala Lys
47   35           40           45
48 Phe Asp Ala Pro Pro Glu Ala Val Ala Ala Lys Leu Gly Val Lys Arg
49   50           55           60
50 Cys Thr Asp Gln Met Ser Leu Gln Lys Arg Ser Leu Ile Ala Glu Val
51   65           70           75           80
52 Leu Val Lys Ile Leu Lys Lys Cys Ser Val
53   85           90
55 <210> SEQ ID NO: 3
56 <211> LENGTH: 95
57 <212> TYPE: PRT
58 <213> ORGANISM: Homo sapien
60 <400> SEQUENCE: 3

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61 Met Lys Leu Leu Met Val Leu Met Leu Ala Ala Leu Leu Leu His Cys
62 1 5 10 15
63 Tyr Ala Asp Ser Gly Cys Lys Leu Leu Glu Asp Met Val Glu Lys Thr
64 20 25 30
65 Ile Asn Ser Asp Ile Ser Ile Pro Glu Tyr Lys Glu Leu Leu Gln Glu
66 35 40 45
67 Phe Ile Asp Ser Asp Ala Ala Ala Glu Ala Met Gly Lys Phe Lys Gln
68 50 55 60
69 Cys Phe Leu Asn Gln Ser His Arg Thr Leu Lys Asn Phe Gly Leu Met
70 65 70 75 80
71 Met His Thr Val Tyr Asp Ser Ile Trp Cys Asn Met Lys Ser Asn
72 85 90 95
74 <210> SEQ ID NO: 4
75 <211> LENGTH: 508
76 <212> TYPE: DNA
77 <213> ORGANISM: Homo sapien
79 <400> SEQUENCE: 4
80 ctgccacgca cgactgaaca cagacagcag ccgcctcgcc atgaagctgc tgaaggctcc 60
81 catgctggcg gccctcctcc tgcactgcta tgcagattct ggctgcaaac tcctggagga 120
82 catggttgaa aagaccatca attccgacat atctatacct gaatacaaa agcttcttca 180
83 agagttcata gacagtgatg ccgctgcaga ggctatgggg aaattcaagc agtgtttcc 240
84 caaccagtca catagaactc tgaaaaactt tggactgatg atgcatacag tgtacgacag 300
85 catttggtgt aatatgaaga gtaattaaat ttaccacaag cgtttkgctc agagggctac 360
86 agactatggc cagaactcat ctgttgattg ctagaaacca cttttcttcc ttgtgtgtgc 420
87 tttttatgtg gaaactgcta gacaactgtt gaaacctcaa attcatttcc atttcaataa 480
88 actaactgca aatcactaga aaaaaaaaa 508
90 <210> SEQ ID NO: 5
91 <211> LENGTH: 381
92 <212> TYPE: DNA
93 <213> ORGANISM: Homo sapien
95 <400> SEQUENCE: 5
96 ggtcgaaatcc aaatcactca ttgtgaaagc tgagctcaca gccgaataag ccaccatgag 60
97 gctgtcagtg tgtctcctga tggctctgct ggccctttgc tgcataccagg cccatgctct 120
98 tgtctgcccc gctgttgctt ctgagatcac agtcttctta ttcttaagtg acgctgcggg 180
99 aaacctccaa gttgccaaac ttaatccacc tccagaagct cttgcagcca agttggaagt 240
100 gaagcactgc accgatcaga tatcttttaa ggaacggctc tcattgaaaa agtctctggg 300
101 gggaatagtg aaaaaatgtg gtgtgtgaca tgtaaaaaatg ctcaacctgg gtttcmarg 360
102 tcttttcaac ggcaacctga t 381
104 <210> SEQ ID NO: 6
105 <211> LENGTH: 508
106 <212> TYPE: DNA
107 <213> ORGANISM: Homo sapien
109 <400> SEQUENCE: 6
110 gggcaagtgg aacctatggc ttggtggatt ttgctagatt tttctgattt ttaaactcct 60
111 gaaaaatatc ccagataact gtcataaagc tggtaactat cttctgtctg gtgacctatc 120
112 gcctttgtag ttactctgct actgccttcc tcatcaacaa agtgccctt cctgttgaca 180
113 agttggcacc ttactctctg gacaacattc ttccctttat ggatccatta aagcttcttc 240
114 tgaaaactct gggcatttct gttgagcacc ttgtggaggg gctaaggagg tgtgtaaatg 300
115 agctgggacc agaggcttct gaagctgtga agaaactgct ggaggcgcta tcacacttgg 360

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116 tgtgacatca agataaagag cggaggtgga tggggatgga agatgatgct cctatcctcc 420
 117 ctgcctgaaa cctgttctac caattataga tcaaatgccc taaaatgtag tgaccctgta 480
 118 aaaggacaaa taaagcaatg aatacatt 508
 120 <210> SEQ ID NO: 7
 121 <211> LENGTH: 93
 122 <212> TYPE: PRT
 123 <213> ORGANISM: Homo sapien
 125 <400> SEQUENCE: 7
 126 Met Lys Leu Val Thr Ile Phe Leu Leu Val Thr Ile Ser Leu Cys Ser
 127 1 5 10 15
 128 Tyr Ser Ala Thr Ala Phe Leu Ile Asn Lys Val Pro Leu Pro Val Asp
 129 20 25 30
 130 Lys Leu Ala Pro Leu Pro Leu Asp Asn Ile Leu Pro Phe Met Asp Pro
 131 35 40 45
 132 Leu Lys Leu Leu Lys Thr Leu Gly Ile Ser Val Glu His Leu Val
 133 50 55 60
 134 Glu Gly Leu Arg Lys Cys Val Asn Glu Leu Gly Pro Glu Ala Ser Glu
 135 65 70 75 80
 136 Ala Val Lys Lys Leu Leu Glu Ala Leu Ser His Leu Val
 137 85 90
 139 <210> SEQ ID NO: 8
 140 <211> LENGTH: 562
 141 <212> TYPE: DNA
 142 <213> ORGANISM: Homo sapien
 144 <400> SEQUENCE: 8
 W--> 145 gcagggtttt ctcagggtcg cgggagggc cggcgctgga ggggagagga cgggtataa 60
 146 gaagcctcgt ggccttgccc gggcagccgc aggttccccg cgcgccccga gccccgcgc 120
 147 catgaagctc gccgccctcc tggggctctg cgtggccctg tctgcagct ccgctgytgc 180
 148 ttctctagtg ggtcgggcca agcctgtggc ccagcctgtc gctgcgctgg agtcggcggc 240
 149 ggaggccggg gccgggaccc tggccaaccc cctcggcacc ctcaaccgcg tgaagctcct 300
 150 gctgagcagc ctgggcatcc ccgtgaacca cctcatagag ggtccccaga agtgtgtggc 360
 151 tgagctgggt cccagggccg tgggggccgt gaaggccctg aaggccctgc tgggggccct 420
 152 gacagtgttt ggctgagccg agactggagc atctacacct gaggacaaga cgctgccac 480
 153 ccgcgagggc tgaatacccc gccgcgggga ggaccgtcca tcccttccc ccggccccctc 540
 154 tcaataaacg tggtaagag ca 562
 156 <210> SEQ ID NO: 9
 157 <211> LENGTH: 104
 158 <212> TYPE: PRT
 159 <213> ORGANISM: Homo sapien
 161 <400> SEQUENCE: 9
 162 Met Lys Leu Ala Ala Leu Leu Gly Leu Cys Val Ala Leu Ser Cys Ser
 163 1 5 10 15
 164 Ser Ala Val Ala Phe Leu Val Gly Ser Ala Lys Pro Val Ala Gln Pro
 165 20 25 30
 166 Val Ala Ala Leu Glu Ser Ala Ala Glu Ala Gly Ala Thr Leu Ala
 167 35 40 45
 168 Asn Pro Leu Gly Thr Leu Asn Pro Leu Lys Leu Leu Ser Ser Leu
 169 50 55 60
 170 Gly Ile Pro Val Asn His Leu Ile Glu Gly Ser Gln Lys Cys Val Ala

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171 65          70          75          80
172 Glu Leu Gly Pro Gln Ala Val Gly Ala Val Lys Ala Leu Lys Ala Leu
173          85          90          95
174 Leu Gly Ala Leu Thr Val Phe Gly
175          100
177 <210> SEQ ID NO: 10
178 <211> LENGTH: 90
179 <212> TYPE: PRT
180 <213> ORGANISM: Homo sapien
182 <400> SEQUENCE: 10
183 Met Arg Leu Ser Val Cys Leu Leu Met Val Ser Leu Ala Leu Cys Cys
184 1          5          10          15
185 Tyr Gln Ala His Ala Leu Val Cys Pro Ala Val Ala Ser Glu Ile Thr
186          20          25          30
187 Val Phe Leu Phe Leu Ser Asp Ala Ala Val Asn Leu Gln Val Ala Lys
188          35          40          45
189 Leu Asn Pro Pro Pro Glu Ala Leu Ala Ala Lys Leu Glu Val Lys His
190          50          55          60
191 Cys Thr Asp Gln Ile Ser Phe Lys Glu Arg Leu Ser Leu Lys Lys Ser
192          65          70          75          80
193 Trp Val Gly Ile Val Lys Lys Cys Gly Val
194          85          90
197 <210> SEQ ID NO: 11
198 <211> LENGTH: 68
199 <212> TYPE: DNA
200 <213> ORGANISM: Artificial Sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION: Restriction site
205 <400> SEQUENCE: 11
206 agctcggaat tccgagcttg gatcctctag agcggccgcc gactagttag ctgctcgacc 60
207 cggaatt 68
209 <210> SEQ ID NO: 12
210 <211> LENGTH: 68
211 <212> TYPE: DNA
212 <213> ORGANISM: Artificial Sequence
W--> 214 <220> FEATURE:
W--> 214 <223> OTHER INFORMATION:
214 <400> SEQUENCE: 12
215 aattaattcc cgggtcgacg agctcactag tcggcgccg ctctagagga tccaagctcg 60
216 gaattccg 68

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see item 12 on Ena Summary sheet

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:145 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:145 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:145 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:145 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:145 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
L:214 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:214 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: